Amendments To The Specification

Please replace paragraph [0017] (Figure 1 legend), page 6 in the application as filed, with the following amended version of that paragraph:

[0017] FIG. 1 depicts the SARS-associated coronavirus genome (SEQ ID NOS:40-43, respectively in order of appearance) and various primers (SEQ ID NOS:27, 19, 28-29, 21, 23, 30-31, 11, 13, 32, 14, 16, 33, 8, 4, 34, 6 and 35-39, respectively in order of appearance).

Please replace the text of paragraph [0050], page 16 in the application as filed, with the following amended version of that paragraph:

[0050] The primers from Canada are set forth below:

First PCR:

5'-CAg AgC CAT gCC TAA CAT g (SEQ ID NO:17)

5'-AAT gTT TAC gCA ggT AAg Cg (SEQ ID NO:18)

Second (Nested) PCR:

5'-TgT TAA ACC Agg Tgg AAC (SEQ ID NO:19)

5'-CCT gTg TTg TAg ATT gCg (SEQ ID NO:20)

Please replace the text of paragraph [0051], page 16 in the application as filed, with the following amended version of that paragraph:

[0051] The primers from Germany are set forth below:

First PCR:

BNIoutS2 5'-ATg AAT TAC CAA gTC AAT ggT TAC (SEQ ID NO:21)

BNIoutAs 5'-CAT AAC CAg TCg gTA CAg CTA C (SEQ ID NO:22)

Second (nested) PCR:

BNIinS 5'-gAA gCT ATT CgT CAC gTT Cg (SEQ ID NO:23)

BNIinAs 5'-CTg TAg AAA ATC CTA gCT ggA g (SEQ ID NO:24)

Please replace the text of paragraph [0055], page 19 in the application as filed, with the following amended version of that paragraph:

[0055] Primers and probe were selected in the N (nucleocapsid protein) gene region at the 3' end of the SARS-CoV genome by using Primer Express Software (PE Applied Biosystems, Foster City, Calif.). The primer set used was: Taq-772F 5'-AAGCCTCGCCAAAAACGTAC (SEQ ID NO:14) (forward) and Taq-1000R 5'-AAGTCAGCCATGTTCCCGAA (SEQ ID NO:15) (reverse), Taq-955T 5'-FAM-TCACGCATTGGCATGGAAGTCA- CAC-T-TAMRA (SEQ ID NO:16) (probe), labeled with the reporter FAM (6-carboxyfluorescein) and the quencher TAMRA (6-carboxytetramethylrhodamine) (TIB Molbiol, Berlin, Germany).

Please amend the text of paragraph [0056], page 19 in the application as filed, as follows:

[0056] A calibration standard was generated by PCR amplification of a 1,277-hp fragment composing part of the N open reading frame (ORF) and the 3' noncoding region (Co-STND-U275, 5'-CCCGACGAGTTCGTGGTGGTG (SEQ ID NO:25); Co-STND-L1529, 5'-GCGTTACACATTAGGGCTCTTC CATA (SEQ ID NO:26). The product was cloned into vector pGEM-Teasy (Invitrogen, Carlsbad, Calif.), and serial dilutions of linearized plasmid were used to optimize the assay. RNA standards were generated by in vitro transcription of linearized plasmid DNA using a mMESSAGE mMACHINE T7 kit as recommended by the manufacturer (Ambion, Austin, Tex.). A portion of the construct (nucleotides 682-1105 of the N ORF) was modified through site-directed mutagenesis, to distinguish plasmid-derived products from authentic products in diagnostic applications. Mutations introduced were an A to G change at position 845 of the N ORE and an A to C change at position 866, creating a unique ApaI restriction site.